



Figure 5: SDS-PAGE showing expression of HAL in *E. coli*.

Lanes:

1 2X 3Z 4 B A

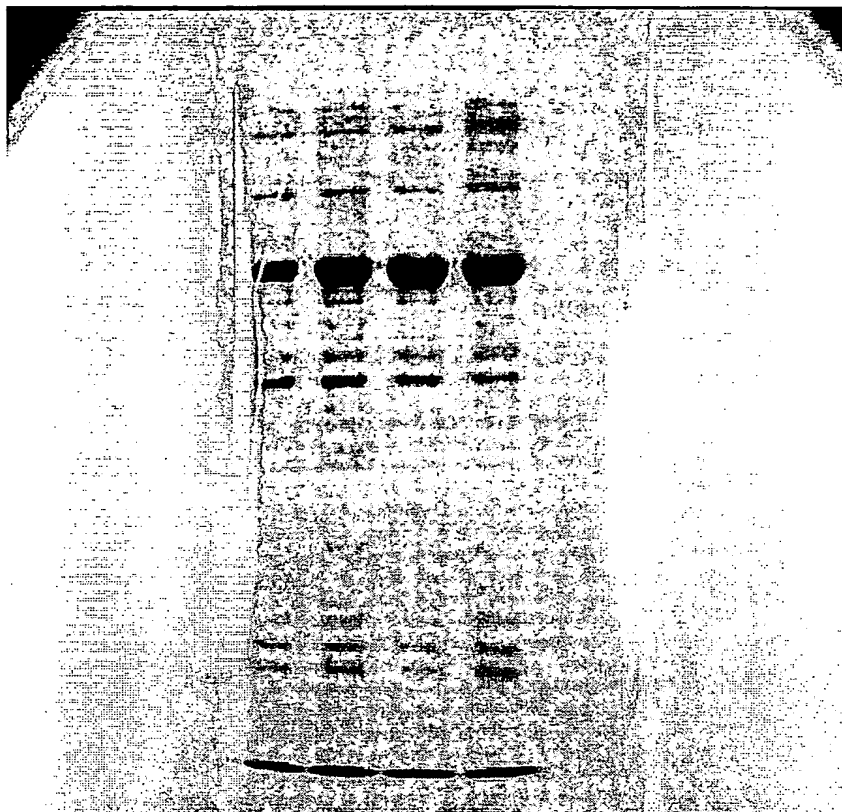
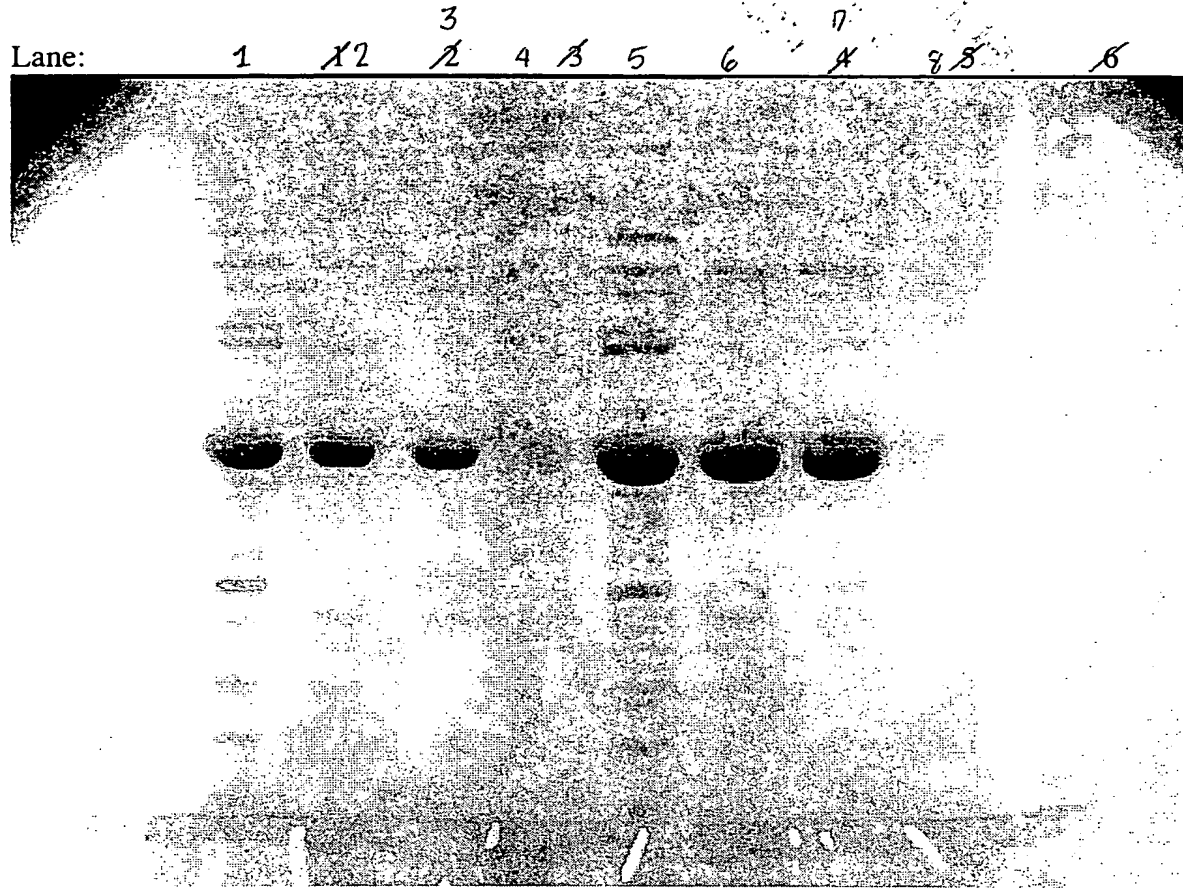




Figure 6: SDS-PAGE showing purification of HAL from *E. coli*





A
Figure 13: Histidine ammonia lyase peptide sequence pileup

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HUTH_PSEPU -----
-
HUTH_RHIME -----
-
HUTH_MOUSE
MPRYTVHVRGEWLAVPCQDGKLTVGWLGREAVRRYMKNKPDNGGFTSVDEVQFLVHRCKG
HUTH_RAT
MPRYTVHVRGEWLAVPCQDGKLSVGWLGREAVRRYMKNKPDNGGFTSVDEVRFVLRCKG
HUTH_HUMAN
MPRYTVHVRGEWLAVPCQDAQLTVGWLGREAVRRYIKNKPDNGGFTSVDDAHFLVRRCKG
HUTH_CAEEL -MRLQVQIGTECVVVPCKP-DDTIHAVAKKSVEKLRLRPK----
LPLADDYFEVRRTVG
HUTH_BACS -----
-
HUTH_STRGR -----
-
HUTH_CORY -----
-

HUTH_PSEPU -----
-
HUTH_RHIME -----
-
HUTH_MOUSE LGLLDNEDELEVALEDNEFVEVVIEGDVMS-----PDFIPSQPEGVFLYSKYR---
-
HUTH_RAT LGLLDNEDLLEVALEDNEFVEVVIEGDVMS-----PDFIPSQPEGVFLYSKYR---
-
HUTH_HUMAN LGLLDNEDRLEVALENNEFVEVVIEGDAMS-----PDFIPSQPEGVFLYSKYR---
-
HUTH_CAEEL
NSLLDPEDLVSDVLKDSDFIIVAASVEETEDAKEAKKQEEIDNARAEIEKIDNRRRKVSF
HUTH_BACS -----
-
HUTH_STRGR -----
-
HUTH_CORY -----
-

HUTH_PSEPU -----
TELTLPKPGTLTLAQLRAIHAAPVRLQLDASAAPIDASVACVEQIIA
HUTH_RHIME -----
MTVILRPGSVPLSDLETIYWTGAPARLDAAFDAGIAKAAARIAEIVA
HUTH_MOUSE -----
EPEKYIALDGDSLSTEDLVNLGKGGRYKIKLTSIAEKKVQQSREVIDSIK
HUTH_RAT -----
EPEKYIALDGDSLSTEDLVNLGKGGRYKIKLTSIAEKKVQQSREVIDSIK
HUTH_HUMAN -----
EPEKYIELDGDRLTEDLVNLGKGGRYKIKLTPAEKRVQKSREVIDSIK
HUTH_CAEEL
ADSLAPMVLAPPTKLLILDGNSLLPEDLVRCEKGECAIQLSMESEDRIRKARTFLEKIAS
HUTH_BACS -----
MVTLDGSSLTTADVAVRLFDFEEAAASEESMERVKKSRAAVERIVR
HUTH_STRGR -----
MDMHTVVVGTSGTTAEDVVAVARHGARVELSAAAVEALAAARLIVDALAA
HUTH_CORY -----
MASAPQITLGLSGATADDVIAVARHEARISISQVLEELASVRAHIDALAS
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^B
Figure 13 cont'd.

HUTH_PSEPU
EDRTAYGINTGFGLLASTRIASHDLENLQRSVLVLSHAAGIGAPLDDDLVRLIMVLKINSL
HUTH_RHIME
GNAPVYGINTGFGLASIKIDSSDVATLQRNLILSHCCGVGQPLTEDIVRLIMALKLISL
HUTH_MOUSE
ERTVVYGITTGFGEKARTVIPANKLQELQVNLVRSHSSGVGKPLSPERCRLMLLRINVL
HUTH_RAT
ERTVVYGITTGFGEKARTVIPANKLQELQVNLVRSHSSGVGKPLSPERCRLMLLRINVL
HUTH_HUMAN
EKTVVYGITTGFGEKARTVIPANKLQELQVNLVRSHSSGVGKPLSPERCRLMLLRINVL
HUTH_CAEEL
EHRVYGVTTGFTFSNV TIPPEKLKKLQNLIRSHATGYGEPLAPNRARMMLLRINIL
HUTH_BACS
DEKTIYGINTGFGEKFSVLIQKEDSAALQLNLILSHACGVGDPFPECVSRAMLLLRANAL
HUTH_STRGR
KPEPVYGVSTGFALASRHIGTELRAQLQRNIVRSHAAGMGPVEREVVRALMFLRLKTV
HUTH_CORY
ADTPVYGISTGFALATRHIAPEDRAKLQRSILIRSHAAGMGEPVEREVVRALMFLRAKTL

HUTH_PSEPU
SRGFSGIRRKVIDALIALVNAEVYPHILPKGSVGASGDLAPLATMSLVLLGEGKARYKGQ
HUTH_RHIME
GRGASGVRLELVRLIEAMLDKGVIPILPEKGSVGASGDLAPLAHMAAVMMGHGEAFFAGE
HUTH_MOUSE
AKGYSGISLETCLKQVIEAFNASCLSYVPEKGTVGASGDLAPLSHLALGLIGEGKMWSPKS
HUTH_RAT
AKGYSGISLETCLKQVIEFNASCLSYVPEKGTVGASGDLAPLSHLALGLIGEGKMWSPKS
HUTH_HUMAN
AKGYSGISLETCLKQVIEMFNASCLPYVPEKGTVGASGDLAPLSHLALGLVGEKGMWSPKS
HUTH_CAEEL
AKGHSGISVENIKKMIAAFNAFCVSYVPQQGTVGCSGDLCPALHLALGLLGEGKMWSPTT
HUTH_BACS
LKGFSGVRAELIEQLLAFLNKRVPVPIQQGSLGASGDLAPLSHLALALIGQGEVFFEGE
HUTH_STRGR
ASGHTGVRPEVAQTMADVLNAGITPVVHEYGSLGCSGDLAPLSHCALTLMGEGEAEGPDG
HUTH_CORY ASGRS-
VRPVVLETMVGMLNAGITPVVREYGSLGCSGDLAPLSHCALVLMGEGEATDAHG

HUTH_PSEPU -
WLSATEALAVAGLEPLTLAAKEGLALLNGTQASTAYALRGLFYAEDLYAAAIACGGLSV
HUTH_RHIME -
RMKGDAALKAAGLSPVTLAAKEGLALINGTQVSTALALAGLFRAHRAGQAALITGALST
HUTH_MOUSE
GWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITS LGCEALERASAIARQADIVAALT
HUTH_RAT
GWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITS LGCEAVERASAIARQADIVAALT
HUTH_HUMAN
GWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITS LGCEAVERASAIARQADIVAALT
HUTH_CAEEL
GWQFADVVLLKKNLEPLELGPKEGLALINGTQMVTALGAYTLERAHNIARQADVIAALS
HUTH_BACS -
RMPAMTGLKKAGIQPVTLSKEGLALINGTQAMTAMGVVAYIEAEKLAYQTERIASLTI
HUTH_STRGR
TVRPAGELLAAGHIAPVELREKEGLALLNGTDGMLGMLVLMALADLRNLYTSADITAALS
HUTH_CORY
DIRPVPELFAEAGLTPVELAEKEGLALVNGTDGMLGQLIMALADLDELDDIADATAAMSV



Figure 13 cont'd.

HUTH_PSEPU EAVLGSRSPFDARIHE-ARGQRGQIDTAACFRDLLGDSSEVSLSHKNCD----
KVQDPYS
HUTH_RHIME DAAMGSSAPFHPDIQH-CAAIRARSTRAAALRQLLTG-SPIRQSHIEGDE---
RVQDPYC
HUTH_MOUSE EVLKGTTKAFDTDIHA-VRPHRGQIEVAFRFRSLDS-
DHHPSEIAESHRCFCDRVQDAYT
HUTH_RAT EVLKGTTKAFDTDIHA-VRPHRGQIEVAFRFRSLDS-
DHHPSEIAESHRCFCDRVQDAYT
HUTH_HUMAN EVLKGTTKAFDTDIHA-LRPHRGQIEVAFRFRSLDS-
DHHPSEIAESHRCFCDRVQDAYT
HUTH_CAEEL DVLKGTTRAYDPDIHR-IRPHRGQNLALRLRALLHS-
EANPSQIAESHNRCTKVQDAYT
HUTH_BACS EGLQGIIDAFDEDIHL-ARGYQEQIDVAERIRFYLS-GLTTSQGE-----
LRVQDAYS
HUTH_STRGR EALLGTDKVLAPELHA-IRPHPGQGVSAADNMSRVLAG-SGLTGHHQDDAP---
RVQDAYS
HUTH_CORY EAQLGTDQVFRAELHEPLRPHPGQGRSAQNMFAFLAD-SPIVASHREGDG---
RVQDAYS

HUTH_PSEPU
LRCQPQVMGACLTQLRQAAEVLGIEANAVSDNPLVFAAEGDVISGGNFHAEPPVMAADNL
HUTH_RHIME IRCQPQVDGACLDLLRSVAATLTIEANAVTDNPLVLSN-
SVVSGGNFHAEPVAFADQI
HUTH_MOUSE
LRCCPQVHGVVNDTIAFVKDIITTELNSATDNPMVFASRGETISGGNFHGEYPAKALDYL
HUTH_RAT
LRCCPQVHGVVNDTIAFVKDIITTELNSATDNPMVFASRGETISGGNFHGEYPAKALDYL
HUTH_HUMAN
LRCCPQVHGVVNDTIAFVKNIITTELNSATDNPMVFANRGETVSGGNFHGEYPAKALDYL
HUTH_CAEEL
LRCVPQVHGVVHDTIEFVREIITTEMNSATDNPLVFADREEIISGGNFHGEYPAKALDFL
HUTH_BACS
LRCIPQVHGATWQTLGYVKEKLEIEMNAATDNPLIFNDGDKVISGGNFHGQPIAFAMDFL
HUTH_STRGR VRCAPQVNGAGRDTLDAALVAGRELASSVDNPPVLPDG-
RVESNGNFHGAPVAYVLDL
HUTH_CORY LRCSPOVTGAARDTIAHARLVATRELAAAIDNPVVLPSG-
EVTSNGNFHGAPVAYVLDL

HUTH_PSEPU ALAIAEIGSLSERRISLMDKHMS-
QLPPFLVENGGVNSGFMIAQVTAALASENKALSH
HUTH_RHIME
ALAVCEIGAISQRIALLVDPALSLRLPAFLAKKPGLSGLMIAEVTSAALMSENKQLSH
HUTH_MOUSE AIGVHELAAISERRIERLCNPSLS-
ELPAFLVAEGGLNSGFMIAHCTAAALVSESKALCH
HUTH_RAT AIGVHELAAISERRIERLCNPSLS-
ELPAFLVAEGGLNSGFMIAHCTAAALVSESKALCH
HUTH_HUMAN AIGIHELAAISERRIERLCNPSLS-
ELPAFLVAEGGLNSGFMIAHCTAAALVSESKALCH
HUTH_CAEEL AIAVAELAQMSERRRLRVNPKLS-
GLPTFLTPDGGLNSGFMFTVQLCAASLVSENKVLCH
HUTH_BACS KIAISELANIAERRIERLVNPQLN-
DLPPFLSPHPGLQSGAMIMQYAAASLVSENKTLAH
HUTH_STRGR
AIVAADLGSICERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTQAALVSEMKRLAV
HUTH_CORY
AIVAADLGSIAERRTDRLMDPARSRDLPAFLADDPGVDSGMMIAQYTQAGLVAENKRLAV



^D
Figure 13 cont'd.

HUTH_PSEPU PHSVDSLPTSANQEDHVSMAPAAGKRLWEMAENTRGVPAIEWLGACQGLDLRKG-LKTS
HUTH_RHIME PASVDSTPTSANQEDHVSMACHGARRLLQMTENLFSIIGIEALAAVQGIEFRAP-LTTS
HUTH_MOUSE PSSVDSLSTSAATEDHVSMGGWAARKALRVVEHVEQVLAIELLAACQGIEFLRP-LKTT
HUTH_RAT PSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRP-LKTT
HUTH_HUMAN PSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRP-LKTT
HUTH_CAEEL PSSVDSIPTSCNQEDHVSMGGFAARKALTVEHVEAVLAMELLAACQGIEFLKP-LIST
HUTH_BACS PASVDSIPSSANQEDHVSMGTIAARHAYQVIANTRRVTAIEAICALQAVEYRGI-EHAA
HUTH_STRGR PASADSI PSSAMQEDHVSMGWSAARKLRTAVDNLARIVAVELYAATRAIELRAAEG LTPA
HUTH_CORY PA-VDSIPSSAMQEDHVSLGWHAARKLPTSVANLRRILAVEMLIAGRALDLRAP-LKPG

HUTH_PSEPU AKLEKARQALRSEVA-HYDRDRFFAPDIEKAVELLAKG---S-LTG LLLPAGVLPSL---
-
HUTH_RHIME PELQKAAA VRGVSS-SIEEDRYMADDLKAAGDLVASG---R-LAAAVSAGILPKLEN-
HUTH_MOUSE TPLEKVYDLVRSVVR-
PWIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEKYRMEHIPESR
HUTH_RAT TPLEKVYDLVRSVVR-
PWIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEKYRMEHIPESR
HUTH_HUMAN TPLEKVYDLVRSVVR-
PWIKDRFMAPDIEAAHRLLEQKVWEVAAPYIEKYRMEHIPESR
HUTH_CAEEL APLHKIYQLVRSVAP-
PLNEDRYMKPEIDAVLEMIRENRIWEAVLPHLETLEAMEELDPD
HUTH_BACS SYTKQLFQEMRKVVP-SIQQDRVFSYDIERLTDWLKK----ESLIPDHQNKELRGMNI-
HUTH_STRGR PASEAVVAALRAAGAEGPGPDRFLAPDLAAADTFVREG---R-LVA AVEPVTGPLA---
-
HUTH_CORY PATGAVLEVLRSKVA-GPGQDRFLSAELEAAAYDLLANG---S-VHKALEAHLPE-----
-

HUTH_PSEPU -----
HUTH_RHIME -----
HUTH_MOUSE PLSPTAFSLES LRKNSATIPESDDL----
HUTH_RAT PLSPTAFSLES LRKNSATIPESDDL----
HUTH_HUMAN PLSPTAFSLQFLHKKSTKIPESEDL----
HUTH_CAEEL ALRQFTKTPTGIVQDRSMIPISDDEESIE
HUTH_BACS -----
HUTH_STRGR -----
HUTH_CORY -----

Figure 14 A

983831	100.0%	1	MASAPQITLGLSGATADVVAVARHARISISPOVLEELASVRAHIDALASADTPVYGISGFGALATRHIAPEBRAKLO	80
1 SWALL: CAC21618	66.1%		-----MHTVVGTSGVTSADVAVARAGARIELSEEAVALAARSVDALAAKPDVYGVSTGFGALATRHISPELRGRLO	
2 SWALL: HUTH_STRGR	65.4%		-MDMHTVVGTSGTAAEDVVAVARHARGARVELSAAAEALAAARLIVDALAAKPEPVYGVSTGFGALASRHIGTELRAQLO	
3 SWALL: HUTH_DEIRA	46.8%		-----MILDRDLNLEQFISVVRHGEQVELSAAARERARARTVIEQIVEGDTPYGVNTGFGKFNQVQIDRSQLAQLO	
4 SWALL: BAB16159	42.0%		-----VPLHHLADIYWNNGSAKLDPSFDAAVLKAARIAEIAAGNAPVYGINTEGFKLASIKIDAAADLATLO	
5 SWALL: Q9KWE4	42.0%		-----VPLHHLADIYWNNGSAKLDPSFDAAVLKAARIAEIAAGNAPVYGINTEGFKLASIKIDAAADLATLO	
6 SWALL: HUTH_BACSU	40.4%		-----MVTLDGSSLTADVARVLDFEEAAASESMERVKKSRAAVERIVRDEKTIYGINTEGFKFSDVLIQKEDSAALO	
7 SWALL: Q9KSQ4	42.2%		-----MLHLMIKPGQLSLKQLRQVSRSPVLSLDPEAIPAIASQAQVVEQVISEGRTVYGINTEGFGLLANTKIAPODLETLQ	
8 SWALL: Q9HU85	41.7%		-----MSLHLKPGQLTLADLRQAYLAPVRLSLDPSADAPIAASVACVENIIAEGRTAYGINTEGFGLLASTRISPADLEKLO	
9 SWALL: Q9KBE6	39.3%		-----MTNLKLLDGRSLSLDHLHRIIYEGETVGASDESMKVKQSRKAVEQIVADEKIIYGITGFGKFSDFIDPDDEVNLO	
10 SWALL: HUTH_PSEPU	41.7%		-----TELTLPKGTTLTQAOLRAHAAPVRLQDASAPDAIDASVACVEQIIAEDRTAYGINTEGFGLLASTRIASHDLENLO	
11 SWALL: HUTH_RHIME	40.6%		-----LTPGSVPLSDLETIYWTGAPARLDAAFDAGIAKAAARIAEIVAGNAPVYGINTEGFKLASIKIDSSDVATLO	
12 SWALL: Q9HU90	40.7%		MSDLPVVFQDGPLRQELVAVARHGARLELSAAAWARIDNARAIVCRIVANGERAYGISTGLGALCDVLLLEGEOIAELS	
13 SWALL: HUTH_HUMAN	39.2%		KYREPEKYIELDGLTTEDLVNLGKGGRYKIKLTPTAEKRVQKSREVIDSIIKEKTVVYGITGFGKFA-RTVIPINKLQLO	
14 SWALL: HUTH_CAEEL	38.8%		VLAAPTLLILDGNSPEDLVRCCKGECATQLSMESDRIRKARTFLEKIASEHRAVYGVTTGFGTFSNVTIIPPEKLKKLO	
15 SWALL: Q9HLI6	41.0%		-----MIEIDGRSLRYEDVYAVAVEYDRVSISSDRTLKAVEEKHEAFLKINSKTVYGVNTGFGSLLNHVIERDQEILO	
16 SWALL: HUTH_MOUSE	38.6%		KYREPEKYIALDGDSTEDLVNLGKGGRYKIKLTSIAEKKVQKSREVIDSIIKERTVVYGITGFGKFA-RTVIPANKLQLO	
17 SWALL: BAB29407	38.6%		KYREPEKYIALDGDSTEDLVNLGKGGRYKIKLTSIAEKKVQKSREVIDSIIKERTVVYGITGFGKFA-RTVIPANKLQLO	
18 SWALL: HUTH_RAT	38.2%		KYREPEKYIALDGDSTEDLVNLGKGGRYKIKLTSIAEKKVQKSREVIDSIIKERTVVYGITGFGKFA-RTVIPANKLQLO	
19 SWALL: AAG53586	39.8%		-----MNALTLPGTTLTQAOLRQVWQQPLQTLDESHEAINDSVACVEAIVAEGRATAYGINTEGFGLLAQTRIATHDLENLO	
20 SWALL: Q9KKE0	38.9%		-----MGEMISLDGPLTWREIASIAEGASLDLSGPARLRIQAARRIVDALVERGINGYGINTEGFGALCDVVISRENQQAALS	
21 SWALL: Q9HQD5	42.2%		-----MSDTRIDAADREALQ	

Figure 14, cont'd.

	81		160
983831	100.0%	1	RSLSHAAGMGEVEREVVRALMFRAKTLASGRTGVRPPVLTWVGMNLNAGITPVREYSGSLGCGDLAPLSHCALVL
1 SWALL: CAC21618	66.1%		RNIVRSHAAAGMGPVEREVVRALMFRLKTVCSGRTGVRPEVAQTMADVLNAGITPVVHEYSGSLGCGDLAPLSHCALT
2 SWALL: HUTH_STRGR	65.4%		RNIVRSHAAAGMGPVEREVVRALMFRLKTVASGHTGVRPEVAQTMADVLNAGITPVVHEYSGSLGCGDLAPLSHCALT
3 SWALL: HUTH_DEIRA	46.8%		HNLIVSHAIGMGEPLPAEVVRGMLLRAQSLSLGHSGVRVEVELLALNADALPVVPSQGSVGSGDLAPLAHLALGL
4 SWALL: BAB16159	42.0%		RNLIISHCCGVPAPLPENVRRLIMALKLISLGRGASGVRIELIRLIEGMLEKGVIPVPEKGSVGSGDLAPLAHMSATM
5 SWALL: Q9KWE4	42.0%		RNLIISHCCGVPAPLPENVRRLIMALKLISLGRGASGVRIELIRLIEGMLEKGVIPVPEKGSVGSGDLAPLAHMSATM
6 SWALL: HUTH_BACSU	40.4%		LNLIISHACGVGDPFPECVSRAMLLIRANALLKGFSGVRAELIEQLAFLNKRVPVIPPQQGSLGASGDLAPLSHLALAL
7 SWALL: Q9KSQ4	42.2%		KSIVLSHAAGIGELMSDETVRMLMLKINSARGYSGRLEVIQALIELVNNQIYPCVPKKGSGVGSGDLAPLAHMSATM
8 SWALL: Q9HU85	41.7%		RSIVLSHAAGVGEALDDAMVRLVMLLKVNSLARGFSGIRRKVIDALIALINAEVYPHIPLKGSVGSGDLAPLAHMSLVL
9 SWALL: Q9KBE6	39.3%		HNLIIYSHACGVGSPFETVSRMTLVLRANALLKGFSGVRPLVIERLLALVNANIHPVIPPQQGSLGASGDLAPLSHLALVL
10 SWALL: HUTH_PSEPU	41.7%		RSVLVSHAAGIGAPLDDDLVRLIMVLKINSLSRGFSGIRRKVIDALIALVNAEVYPHIPLKGSVGSGDLAPLAHMSLVL
11 SWALL: HUTH_RHIME	40.6%		RNLIISHCCGVOPLTEDIVRLIMALKLISLGRGASGVRLRLIEAMLDKGVIPVPEKGSVGSGDLAPLAHMAAVM
12 SWALL: Q9HU90	40.7%		RNTLLSHACGVGEPLRDEQTRAIICRAVANYSQKSGLDRLSLVEGLLALLNHGITPQVPAQGSVGY---LTHMAHVGI
13 SWALL: HUTH_HUMAN	39.2%		VNLVRSHSSGVGKPLSPERCMLLALRINVLAKYSGISLETTLKQVIEAFNASCLPYVPEKGTGASGDLAPLSHLALGL
14 SWALL: HUTH_CAEEL	38.8%		LNLIIRSHATGYGEPPLAPNRARMLLALRINILAKHSGISVENIKKMAAFNFCVSVYPQQGTVGCGDLAPLAHLALGL
15 SWALL: Q9HLI6	41.0%		KNLIIRSHSSGVGDYLENRYVRIMAVRLNSLAGYSAVSADLLNMVEMLNRDVIPAIPKYGSVGSGDLAPLAHIGLAM
16 SWALL: HUTH_MOUSE	38.6%		VNLVRSHSSGVGKPLSPERCMLLALRINVLAKYSGISLETTLKQVIEAFNASCLSYVPEKGTGASGDLAPLSHLALGL
17 SWALL: BAB29407	38.6%		VNLVRSHSSGVGKPLSPERCMLLALRINVLAKYSGISLETTLKQVIEAFNASCLSYVPEKGTGASGDLAPLSHLALGL
18 SWALL: HUTH_RAT	38.2%		VNLVRSHSSGVGKPLSPERCMLLALRINVLAKYSGISLETTLKQVIEAFNASCLSYVPEKGTGASGDLAPLSHLALGL
19 SWALL: AAG53586	39.8%		RSVLVSHAAGVGEPLDDDLVRLIMVLKINSLARGFSGIRLSVIOALIALVNAGVSVDPKAGSVGSGDLAPLAHMSLTL
20 SWALL: Q9KKE0	38.9%		RNIIISHACGVGDPPLGRVEARAVMAAQIANLTHGYSGRVETAEMLLALNADIIPVPSRGSVGY-----LTHAALVL
21 SWALL: Q9HQD5	42.2%		ANLVRSHAAAGAGSELDTAAVRALLVTRNALAKYSGIRERVRDLVLVGLLNEGVHPVVPVPSRGSVGSGDLAPLAHMSRVL

Figure 14, cont'd.

983831	100.0%	161	240
1 SWALL: CAC21618	66.1%		MGEGEATDAHGDIRVPPELFAEAGLTVPVLAKEGALVNGTGMGLGQIMALADLDELDDIADTAAMSVEAQLGTDQV
2 SWALL: HUTH_STRGR	65.4%		MGEGDAEGPDGTVRPAAGELLAAHGIAPIVELREKEGLALINGTGMGLGMVLMALADLDTLYKSADITAAALTMELIGTDRV
3 SWALL: HUTH_DEIRA	46.8%		MGEGEAEGPDGTVRPAAGELLAAHGIAPIVELREKEGLALINGTGMGLGMVLMALADLNLNLTYSADITAAALSLEALLGTDKV
4 SWALL: BAB16159	42.0%		IGLGDI-EYQGQVRPAADVLAELGSLPVQLQAKGELALINGTQMLGSLALALHDAQVLLGTTANLAAAMTVEARYGSHRP
5 SWALL: Q9KWE4	42.0%		MGEGEAF-YQGVQMFPSKDALAKAGLSPPVLAKEGLALINGTQTSTALALAGLFRHRAAQSAVLTGALSTDAMGSSAP
6 SWALL: HUTH_BACSU	40.4%		MGEGEAF-YQGVQMFPSKDALAKAGLSPPVLAKEGLALINGTQTSTALALAGLFRHRAAQSAVLTGALSTDAMGSSAP
7 SWALL: Q9KSQ4	42.2%		IGQGEVF-FEGERMPAMTGLKKAGIQPVTLTSTKEGLALINGTQAMTAMGVWAYTEAEKLAAYQTERIASLTIEGLQGIIDA
8 SWALL: Q9HU85	41.7%		IGEGQAR-YNGKIIISGLEAMKTAGLEPITLAPKEGLALINGTQASTAFALGFLVAEDLFASATVCGAMSVEAALGSRRP
9 SWALL: Q9KBE6	39.3%		IGESRARH-RGEWLPAAEALAVAGLEPITLAAKEGLALINGTQVSTAYALRGVFEAEEDLFAAATVCGGLSVEAMLGSRAP
10 SWALL: HUTH_PSEPU	41.7%		LGEGEVF-YKGTTKKASFALKEEEIEPITLTAKGELALINGTQAMTAMGVWAYTEAEKLAFAQSEIIASLTMEGLRGIIDA
11 SWALL: HUTH_RHIME	40.6%		LGEKGAR-YKGQWLSATEALAVAGLEPITLAAKEGLALINGTQASTAYALRGVFEAEEDLYAAAACGGLSVEAVLGSRSR
12 SWALL: Q9HU90	40.7%		MHGGEAF-FAGERMKGDAALKA-AGLSPTVLAKEGLALINGTQVSTALALAGLFRHRAAQSAVLTGALSTDAMGSSAP
13 SWALL: HUTH_HUMAN	39.2%		LGIGEV-S-YRGSVVPAALAAEGLATVRLGAKDGLCLVNGTPCMTGLACLDLDAQRLAQWADVIGAMSFEALRGQLAA
14 SWALL: HUTH_CAEEL	38.8%		VGECKMSPKSGWADAKYVLEAHGLKPVILKPKGELALINGTQMITSLGCEAVERASAIARQADIVAAALTLEVLKGTTKA
15 SWALL: Q9HLI6	41.0%		LGECKMSPKSGWADAKYVLEAHGLKPVILKPKGELALINGTQMITSLGCEAVERASAIARQADIVAAALTLEVLKGTTKA
16 SWALL: HUTH_MOUSE	38.6%		MGEKGAF-FEGRMLDSARALEKAGLKPQFKEGVALINGTSFMSGILSIAYMDAHDILENAIRSALLSFEALGGTSKA
17 SWALL: BAB29407	38.6%		IGEGKMSPKSGWADAKYVLEAHGLKPVILKPKGELALINGTQMITSLGCEALERASAIARQADIVAAALTLEVLKGTTKA
18 SWALL: HUTH_RAT	38.2%		IGEGKMSPKSGWADAKYVLEAHGLKPVILKPKGELALINGTQMITSLGCEALERASAIARQADIVAAALTLEVLKGTTKA
19 SWALL: AAG53586	39.8%		IGEGKAR-YRGEWLPAAATLQKAGLAPVTLAAKEGLALINGTQASTAFALRGVFEAEEDLFASAVVCGALTTEAVLGSRRP
20 SWALL: Q9KKE0	38.9%		IGHGSAMQGTTERLSGADAL-ARLGLAPIRLEAKGELSLVNGTPCATGLAALALARTERLEFAWADAAAAMTYE-NLGSQAN
21 SWALL: Q9HQD5	42.2%		IGEGQA-DVAGERMPAAEALAAADLEPVTLOAKEGLALINGTQTTGVAALALVDAERVLSADTAGALTTEVTMTSTTAS



Figure 14₂ cont'd.

983831	241	320
1 SWALL: CAC21618	100.0%	FRAELHEPLRPHGQGRSAQNMFALADSPIVASHREGGRVQDAYSLRCSQVGTGARDTIAHARLVATRELAALIDNP
2 SWALL: HUTH_STRGR	66.1%	LAPELHA-IRPHGQQAASANMAAVLKSGSLTGHQDDAPRVQDAYSVRCAPQVAGAGRTDMAHAGLVAERELAAAVDNP
3 SWALL: HUTH_DEIRA	65.4%	LAPELHA-IRPHGQGVSDNMRSVLGSLTGHQDDAPRVQDAYSVRCAPQVAGAGRTDMAHAGLVAERELAAAVDNP
4 SWALL: BAB16159	46.8%	FQPDV-VGLRPHFGALAVAAELREFLAGSEIAPSHLTGDKVQDAYSLRAVQVHGATDALLASVARTLEIEMNAVTDNP
5 SWALL: Q9KWE4	42.0%	FHPDIHT-LRGHKGQIDAGSALRNLLQGSEIRESHIEGDERVQDPYCIRCPQVDMGACLDLLASVARTLEIEMNAVTDNP
6 SWALL: HUTH_BACSU	42.0%	FHPDIHT-LRGHKGQIDAGSALRNLLQGSEIRESHIEGDERVQDPYCIRCPQVDMGACLDLLASVARTLEIEMNAVTDNP
7 SWALL: Q9KSQ4	40.4%	FDEDIHLA-RGYQEIQIDVAERIRFYLSDSLTTS--QGELRVQDAYSLRCIPQVHGATWQTLGYVKEKLEIEMNAVTDNP
8 SWALL: Q9HU85	42.2%	FDPRIHR-VRGHRQMDAATAYRHLLVSSEIGQSHNCE-KVQDPYSLRCQPVDMGACIQQIRSAAEVLEIEMNAVTDNP
9 SWALL: Q9KBE6	41.7%	FDARIHAA-RGQRGQIDVAAAYRDILLASSEVARSHKCD-KVQDPYSLRCQPVDMGACIQQIRSAAEVLEIEMNAVTDNP
10 SWALL: HUTH_PSEPU	39.3%	FDEQIHFA-RGYVEQVDVARRMESYLQDSQLTT--RQELRVQDAYSLRCIPQVHGATWQTLRYVKEKLEIEMNAVTDNP
11 SWALL: HUTH_RHIME	41.7%	FDARIHEA-RGQRGQIDTAACFRDILLGDSSEVSSHKNCD-KVQDPYSLRCQPVDMGACIQQIRSAAEVLEIEMNAVTDNP
12 SWALL: Q9HU90	40.6%	FHPDIQCHAAIRARSTRAAA-LRQLLTGSPHQSHIEGDERVQDPYCIRCPQVDMGACLDLLASVARTLEIEMNAVTDNP
13 SWALL: HUTH_HUMAN	40.7%	FDAEI-VALKPHGPMQVAAANLRAALLAGSQVLENA--GIRTDALSIRSIPQIHGACRDLAARQIET-ELNSATDNP
14 SWALL: HUTH_CAEEL	39.2%	FDTDIHA-LRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCQPVHGAVVNDTIAFVKNIITTELSATDNP
15 SWALL: Q9HLI6	38.8%	YDPDIHR-IRPHRGQNLALRLRALLNPQIAESHRNCT-KVQDAYTLRCQPVHGAVVNDTIEFVREIITTELSATDNP
16 SWALL: HUTH_MOUSE	41.0%	FTPWILGA-RPHLGQVAIGNRFREYLTGSDIV--KRADSVKVQDAYTLRCIPQVGVGVADVIDYVENVLVEIEMNAVTDNP
17 SWALL: BAB29407	38.6%	FDTDIHA-VRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCQPVHGAVVNDTIAFVKDIITTELSATDNP
18 SWALL: HUTH_RAT	38.6%	FDTDIHA-VRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCQPVHGAVVNDTIAFVKDIITTELSATDNP
19 SWALL: AAG53586	39.2%	FDARIHE-VRGQRGQIDAAALFRHVLTDTSIAASHNCD-KVQDPYSLRCQPVDMGACIQQIRSAAEVLEIEMNAVTDNP
20 SWALL: Q9KKE0	38.9%	AFALPLALRQSPGLSAGEGLRDWLADSPMLAG--TAGTRTQDPLSLRAVQVHGAGARDAFGQVAEIVDRELASVTDNP
21 SWALL: Q9HQD5	42.2%	CAPAIHE-VRPHDGQAVSARHINLTAGSEVLHDHRCDC-RVQDAYSLRCIPQVHGAVRDALDHLRAAVATELSATDNP



Figure 14, cont'd.

	983831	321	400
1	SWALL: CAC21618	100.0%	VVLPSGEVTSNGNFHFCAPVAVYLDFLATAVADLGSIAERRTRDMLDPARSRLPAFLADDPGVDSGMIAQYTOAGLVAE
2	SWALL: HUTH_STRGR	66.1%	VVLPGDRVESNGNFHFCAPVAVYLDFLATAVADLGSIAERRTRDMLDKNRSHGLPFLADDPGVDSGLMIAQYTOAALVGE
3	SWALL: HUTH_DEIRA	65.4%	VVLPGDRVESNGNFHFCAPVAVYLDFLATAVADLGSICERRTRDMLDKNRSHGLPFLADDPGVDSGLMIAQYTOAALVSE
4	SWALL: BAB16159	46.8%	LIFPTGEVVSNGNFHFCAPVAVYLDFLATAVADLGSISERRTEQLLNPLS-GLPAFLTPNGGLNSGFMIAQYTSAAALVSE
5	SWALL: Q9KWE4	42.0%	LVLSDNSVVSNGNFHFCAPVAVYLDFLATAVADLGSIAQRRRIALLVDPALSYGLPAFLSKKPGGLNSGLMIAEVTSAALMSE
6	SWALL: HUTH_BACSU	42.0%	LVLSDNSVVSNGNFHFCAPVAVYLDFLATAVADLGSIAQRRRIALLVDPALSYGLPAFLSKKPGGLNSGLMIAEVTSAALMSE
7	SWALL: Q9KQ4	40.4%	LIFNDGDIISGNGNFHFCAPVAVYLDFLATAVADLGSIAQRRRIALLVDPALSYGLPAFLSKKPGGLNSGLMIAEVTSAALMSE
8	SWALL: Q9HU85	42.2%	LIFADGDIISGNGNFHFCAPVAVYLDFLATAVADLGSIAQRRRIALLVDPALSYGLPAFLSKKPGGLNSGLMIAEVTSAALMSE
9	SWALL: Q9KBE6	41.7%	LIFAAGDVISGNGNFHFCAPVAVYLDFLATAVADLGSIAQRRRIALLVDPALSYGLPAFLSKKPGGLNSGLMIAEVTSAALMSE
10	SWALL: HUTH_PSEPU	39.3%	LIFDNGQVTSNGNFHFCAPVAVYLDFLATAVADLGSIAQRRRIALLVDPALSYGLPAFLSKKPGGLNSGLMIAEVTSAALMSE
11	SWALL: HUTH_RHIME	41.7%	LIFAAGDVISGNGNFHFCAPVAVYLDFLATAVADLGSIAQRRRIALLVDPALSYGLPAFLSKKPGGLNSGLMIAEVTSAALMSE
12	SWALL: Q9HU90	40.6%	LVLSDNSVVSNGNFHFCAPVAVYLDFLATAVADLGSIAQRRRIALLVDPALSYGLPAFLSKKPGGLNSGLMIAEVTSAALMSE
13	SWALL: HUTH_HUMAN	40.7%	LLLTGTPVVSQANPHGESVAMAADLLATAVAELGGVAERRLDRLVNPVS-GLPAFLVKGKPGVNSGMMITQYVAAASLAGE
14	SWALL: HUTH_CAEEL	39.2%	MVFANGETVSGNGNFHFCAPVAVYLDFLATAVADLGSIAQRRRIALLVDPALSYGLPAFLSKKPGGLNSGLMIAEVTSAALMSE
15	SWALL: Q9H16	38.8%	LVPADREIISGNGNFHFCAPVAVYLDFLATAVADLGSIAQRRRIALLVDPALSYGLPAFLSKKPGGLNSGLMIAEVTSAALMSE
16	SWALL: HUTH_MOUSE	41.0%	L-FNGEEVVSNGNFHFCAPVAVYLDFLATAVADLGSIAQRRRIALLVDPALSYGLPAFLSKKPGGLNSGLMIAEVTSAALMSE
17	SWALL: BAB29407	38.6%	MVFASGETISGNGNFHFCAPVAVYLDFLATAVADLGSIAQRRRIALLVDPALSYGLPAFLSKKPGGLNSGLMIAEVTSAALMSE
18	SWALL: HUTH_RAT	38.6%	MVFASGETISGNGNFHFCAPVAVYLDFLATAVADLGSIAQRRRIALLVDPALSYGLPAFLSKKPGGLNSGLMIAEVTSAALMSE
19	SWALL: AAG53586	38.2%	MVFASGETISGNGNFHFCAPVAVYLDFLATAVADLGSIAQRRRIALLVDPALSYGLPAFLSKKPGGLNSGLMIAEVTSAALMSE
20	SWALL: Q9KKE0	39.8%	LVFAANEMVFRNGNFHFCAPVAVYLDFLATAVADLGSIAQRRRIALLVDPALSYGLPAFLSKKPGGLNSGLMIAEVTSAALMSE
21	SWALL: Q9HQD5	38.9%	AVAGSPEVHSQAHAAGLGLAMDSLAVAEVAAISERRIDRLVNPVS-GLPAFLAGDSGVSSGFMIAQYTAALVAE
		42.2%	LVPFSGTVVSNGNFHFCAPVAVYLDFLATAVADLGSIAQRRRIALLVDPALSYGLPAFLSKKPGGLNSGLMIAEVTSAALMSE

Title: CLONING, OVEREXPRESSION AND
THERAPEUTIC USE OF BIOACTIVE
HISTIDINE AMMONIA LYASE
Inventor(s): Joseph ROBERTS et al.
DOCKET NO.: 078728/0106



401	983831	100.0%	NKRLAVPASVDSIPSSAMQEDHVS	LGWHHRAKRLRTSVANLRRLILAVEMLIAGRALDLRALPKPGPATGAVLEVLRSKVAG	
	1	SWALL:CAC21618	66.1%	LKRLAVPASADSIPSSAMQEDHVS	MGWSAARKLRTAVDNLARVIAVELYAAATRAITQLREGLTPAPASQAVVEAVRAAVEG
	2	SWALL:HUTH_STRGR	65.4%	MKRLAVPASADSIPSSAMQEDHVS	MGWSAARKLRTAVDNLARVIAVELYAAATRAIELRAALTTPAPASEAVVAALRAAGAG
	3	SWALL:HUTH_DEIRA	46.8%	NKVLHPASVDSIPTSANQEDHVS	MGHAARQLRQIVANQTVLSIELLCAAQGLDQQ-LRAGRQVQAAYEVYRTFVPT
	4	SWALL:BAB16159	42.0%	NKQMSHPASVDSIPTSANQEDHVS	MACGARRLLAMTDNLFGILGIEALAAVQGVDELGRPLKTSPELEKAAAVLRSAPV
	5	SWALL:Q9KWE4	42.0%	NKQMSHPASVDSIPTSANQEDHVS	MACGARRLLAMTDNLFGILGIEALAAVQGVDELGRPLKTSPELEKAAAVLRSAPV
	6	SWALL:HUTH_BACSU	40.4%	NKTLAHPASVDSIPSSAMQEDHVS	MGTTAARHAYQVIANTRRVIAIEAICALQAVEYRGIEHAASVTKQLFQEMRKVVP
	7	SWALL:Q9KSQ4	42.2%	NKTLAHPASVDSLPTSANQEDHVS	MAFFAARLRDMGENTRGILAVEYLAACQGLDFRAPLKSSPRIEEARQILREKVP
	8	SWALL:Q9HU85	41.7%	NKALAHPASVDSLPTSANQEDHVS	MAPNAGKRLWAMAEENVRCILAVENLGACQGLDFREGILKSSPKLEQAARLLRDKVP
	9	SWALL:Q9KBE6	39.3%	NKTLAHPASVDSIPSSAMQEDHVS	MGTTIGSRHAYQIQIONRVNVAIELICAMQAVDIRGREKMASTFKILEKGREHPV
	10	SWALL:HUTH_PSEPU	41.7%	NKALSHPASVDSLPTSANQEDHVS	MAPAGKRLWEMAENRGVLAIEWLGACQGLDFRAPLKTSAKLEKAQARLRSEVHA
	11	SWALL:HUTH_RHIME	40.6%	NKQIUSHPASVDSIPTSANQEDHVS	MACGARRLLQMENTENLFIIGIEALAAVQGFIEFRAPLTSPELQKAAARLVSS
	12	SWALL:Q9HU90	40.7%	NRQLAQPAVDNFVTSALQEDHLS	LSGLTSAALKLGRALENLRILAIEYLLAAQAFELAPORFGQGTAAAGWILRERVPA
	13	SWALL:HUTH_HUMAN	39.2%	NKALCHPSSVDSLSTSAATEDHVS	MGWGAARKALRVIEHVEQVLAIELLAACOGIEFLRPLKTTTTPLEKVYDLVRSVVRP
	14	SWALL:HUTH_CAEL	38.8%	NKVLCHPSSVDSIPTSCNQEDHVS	MGGAARKALTVVEHVEAVLAMELLAACOGIEFLKPLISTAPLHKIYQLVRS-VAP
	15	SWALL:Q9HLI6	41.0%	NKVLAYPSSADTIPTSANQEDHVS	MGATGSKLLEIIDNVRYIIAIEYLLGSQALEFTDK-GMSPSTRKIYEKIREKVEK
	16	SWALL:HUTH_MOUSE	38.6%	SKALCHPSSVDSLSTSAATEDHVS	MGWGAARKALRVVEHVEQVLAIELLAACOGIEFLRPLKTTTTPLEKVYDLVRSVVRP
	17	SWALL:BAB29407	38.6%	SKALCHPSSVDSLSTSAATEDHVS	MGWGAARKALRVVEHVEQVLAIELLAACOGIEFLRPLKTTTTPLEKVYDLVRSVVRP
	18	SWALL:HUTH_RAT	38.2%	SKALCHPSSVDSLSTSAATEDHVS	MGWGAARKALRVIEHVEQVLAIELLAACOGIEFLRPLKTTTTPLEKVYDLVRSVVRP
	19	SWALL:AAG53586	39.8%	NKGLCHPTSVDK-PPSANQEDHVS	MAPAGRRLLWEMAGNTRGVLAWEVLAACQADLRDGLTSSPLLEQARQSCGEQVAH
	20	SWALL:Q9KKE0	38.9%	NRRLAAPASLDGGITSAQEDML	THATPAAWKALSTIVDNLERILAIELLAHRMCSCKRRARRNAPLPFTCTYARRSP
	21	SWALL:Q9HOD5	42.2%	LRLSGQP-TLDNASVGAQEDHVS	MSAGAAYNFREAVEKAAATVVGBELLCGAQGREFLDPLALGAGTAAAYDLVR-EVSE

Figure 14, cont'd

983831	100.0%	[5	513
1 SWALL: CAC21618	66.1%	PGQDRFLSAELEAAAYDLLANGSVHKALEAHLPA		
2 SWALL: HUTH_STRGR	65.4%	PGPDRHLAPDLAAADAFVRAGHLVAAAESVTGP		
3 SWALL: HUTH_DEIRA	46.8%	PGPDRFLAPDLAAADTFVREGRLVAAVEPVTGP		
4 SWALL: BAB16159	42.0%	LTEDRYFRPDLRLRGELVSGRVAQAADTQAPA		
5 SWALL: Q9KWE4	42.0%	LEDDRYMATDLKAAIEVVASGALVSAISSGLPV		
6 SWALL: HUTH_BACSU	40.4%	LEDDRYMATDLKAAIEVVASGALVSAISSGLPV		
7 SWALL: Q9KSQ4	42.2%	IQQDRVFSYDIERLTDWLKESLIPDHQNKELR		
8 SWALL: Q9HU85	41.7%	YQKDRYFAPDIEKANALL-QLAVHNRLMPDQLL		
9 SWALL: Q9KBE6	39.3%	YQEDRFFAPDIEAASQLLASGCINALLPARLLP		
10 SWALL: HUTH_PSEPU	41.7%	IDQDRMFAKDIERAAKWLKDGSDFTKMKREKER		
11 SWALL: HUTH_RHIME	40.6%	YDRDRFFAPDIEKAVELLAKGSLTGLLPAGLPS		
12 SWALL: Q9HU90	40.7%	IEEDRYMADDLKAAGDLVASGRLAADVAGLPK		
13 SWALL: HUTH_HUMAN	39.2%	YDTRWLAPDIASAAAILGERKSLARLAASIGD		
14 SWALL: HUTH_CAEEL	38.8%	WIKDRFMAPDIEAAHRLLEQKVWEVAAPYIEK		
15 SWALL: Q9HLI6	41.0%	PNEDRYMKPEIDAVLEMIRENRIWEAVLPHLET		
16 SWALL: HUTH_MOUSE	38.6%	LDHDPSPFDIETIRKMMDKKEFISALP-----		
17 SWALL: BAB29407	38.6%	WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK		
18 SWALL: HUTH_RAT	38.2%	WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK		
19 SWALL: AAG53586	39.8%	YDDDRFFAPDIEAAISLNLKGSVLGLLPAFL---		
20 SWALL: Q9KKE0	38.9%	PIATIVR-----		
21 SWALL: Q9HQD5	42.2%	PAGDRALADDMAAVGDLVRAGLVEDAVARALDA		



Figure 14, cont'd.

KEY:

983831 : HAL

1	CAC21618	: Streptomyces coelicolor
2	HUTH_STRGR	: Streptomyces griseus
3	HUTH_DEIRA	: Deinococcus radiodurans
4	BAB16159	: Agrobacterium rhizogenes
5	Q9KWE4	: Agrobacterium rhizogenes
6	HUTH_BACSU	: Bacillus subtilis
7	Q9KSQ4	: Vibrio cholerae
8	Q9HU85	: Pseudomonas aeruginosa
9	Q9KBE6	: Bacillus halodurans
10	HUTH_PSEPU	: Pseudomonas putida
11	HUTH_RHIME	: Rhizobium meliloti
12	Q9HU90	: Pseudomonas aeruginosa
13	HUTH_HUMAN	: Human
14	HUTH_CAEEL	: Caenorhabditis elegans
15	Q9HLI6	: Thermoplasma acidophilum
16	HUTH_MOUSE	: Mouse
17	BAB29407	: Mus musculus (Mouse)
18	HUTH_RAT	: Rat
18	AAG53586	: uncultured bacterium pCosAS1
20	Q9KKE0	: Rhizobium meliloti
21	Q9HQD5	: Halobacterium sp



Figure 15 A.

```
STRG      6  VVVGTSGTTAEDVVAVARHGARVELSAAAVEALAAARLIVDALAAKPEPVYGVSTGFGAL
"HAL"     7  ITLGLSGATADDVIAVARHEARISISPPVLEELASVRAHIDALASADTPVYGISTGFGAL
          *  ** ** ** ** ** ** ** ** ** ** ** **   *  ** **   *  ** **   *  ** **   *  ** **   *  ** **
STRG,    66  ASRHIGTELRAQLQRNIVRSHAAGMPRVEREVVRALMFLRLKTVASGHTGVRPEVAQTM
HAL      67  ATRHIAPEDRAKLQRSIRSHAAGMGEPPEREVVRALMFLRAKTLASGRTGVRPVLVETM
          *  ** ** *  ** **   *  ** **   *  ** **   *  ** **   *  ** **
STRG    126  ADVLNAGITPVVHEYGSLGCSGDLAPLSHCALTLMGEGEAGPDGTVRPAGELLAAHGIA
HAL     127  VGMLNAGITPVVREYGSLGCSGDLAPLSHCALVLMGEGEATDAHGDIRPVPELFAEAGLT
          *  ** ** **   *  ** **   *  ** **   *  ** **   *  ** **
STRG    186  PVELREKEGLALLNGTDMGLMGLVMALADLRNLYTSADITAAALSLEALLGTDKVLAPELH
HAL     187  PVELAEKEGLALVNGTDMGLQLIMALADLDELDDIADATAAMSVEAQLGTDQVFRaelH
          *  ** ** **   *  ** **   *  ** **   *  ** **   *  ** **
STRG    246  A-IRPHPGQGVSAADNMSRVLAGSGLTGHQHDDAPRVQDAYSVRCAPQVNGAGRDTLDHAA
HAL     247  EPLRPHPGQGRSAQNMFALADSPIVASHREGDGRVQDAYSLRCSPPQVTGAARDTIAHAR
          *  ** ** **   *  ** **   *  ** **   *  ** **   *  ** **
STRG    305  LVAGRELASSVDNPVPLPDGRVESNGNFHGAPVAYVLDFLAIVAADLGSICERRTDRLLD
HAL     307  LVATRELAAAIIDNPVPLPSGEVTSNGNFHGAPVAYVLDFLAIAVADLGSIAERRTDRMLD
          *  ** ** **   *  ** **   *  ** **   *  ** **   *  ** **
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20
JUN 03 2003
TEXT & TRADEMARK OFFICE

Title: CLONING, OVEREXPRESSION AND
THERAPEUTIC USE OF BIOACTIVE
HISTIDINE AMMONIA LYASE
Inventor(s): Joseph ROBERTS et al.
DOCKET NO.: 078728/0106

O I P E

Figure 15_B, Cont'd.

STRG	365	KNRSHGLPPFLADDAGVDSGLMIAQYTQAALVSEMKRLAVPASADSI PSSAMQEDHVS	MG
HAL	367	PARSRDLPAFLADDPGVDSGMMIAQYTQAGLVAENKRLAVPASVDSI PSSAMQEDHVS	LG
		** ** *	** ** *
STRG	425	WSAARKLRTAVDNLRIVAVELYAATRAIELRAAEGLT PAPASEAVVAALRAAGAE	GP
HAL	427	WHAARKLRTSVANLRRILAVEMLIAGRALDLRAP--LKPGPATGAVLEVLRSKVA-G	PGQ
		* ** *	* ** *
STRG	485	DRFLAPDLAAADTFVREGRLVAAVE	
HAL	484	DRFLSAELEAAAYDLLANGSVHKALE	
		***	* ** *